

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 17:40:54 ; Search time 43 Seconds
(without alignments)
1798,882 Million cell updates/sec

Title: US-09-635-501-2
Perfect score: 4291
Sequence: 1 MSSSWLLLSLVAVTAQAQT.....ISKGNFPGFQNTDDVQVSF 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	4281	99.8	804	2	T14762
2	1344	31.3	732	1	S05238
3	1337	31.2	1306	1	A31759
4	1334	31.1	732	1	A35655
5	1334	31.1	1312	1	A34171
6	1312	30.6	1193	2	JC2489
7	1310	30.5	1313	1	JC2038
8	1283	29.9	737	1	A34402
9	1283	29.9	1309	1	S35484
10	1058	24.7	611	2	S65472
11	1039	24.2	615	2	A57533
12	1030	24.0	630	2	JC5374
13	642.5	15.0	907	2	T15792
14	157	3.7	532	2	C83696
15	154	3.6	502	2	AF1310
16	147	3.4	502	2	AE1682
17	139.5	3.3	987	2	AI2011
18	139	3.2	608	2	B82938
19	136	3.2	611	2	D82881
20	135	3.1	501	2	D69943
21	125	2.9	627	1	S40048
22	124.5	2.9	987	2	I48373
23	124	2.9	538	2	E72561
24	123.5	2.9	902	2	E90270
25	123	2.9	990	2	S23416
26	122	2.8	642	2	E98000
27	121	2.8	607	2	AB3511
28	121	2.8	1034	2	T30574
29	120	2.8	1339	2	A84683

RESULT 1
T14762
hypothetical protein DKFp434A014.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14762
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A:Reference number: Z18181
A:Accession: T14762
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-804 <WAM>
A:Cross-references: EMBL:AL110224
A:Experimental source: adult testis; clone DKFp434A014
C:Genetics:
A:Note: DKFp434A014.1

Query Match 99.8%; Score 4281; DB 2; Length 804;
Best Local Similarity 99.9%; Pred. No. 6.7e-288;
Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	SSSSWLLLSLVAVTAQAQTIEQAKTFLDKFNHRAEDLFYQSSLASWNYNTNTEENVQN	61
Db	1	SSSSWLLLSLVAVTAQAQTIEQAKTFLDKFNHRAEDLFYQSSLASWNYNTNTEENVQN	60
QY	62	MNAGDKWSAFLKEQSTLAQMYPLQEIQLNLTVKLQALQONGSVLSSEDKSKRLNTILN	121
Db	61	MNAGDKWSAFLKEQSTLAQMYPLQEIQLNLTVKLQALQONGSVLSSEDKSKRLNTILN	120
QY	122	TMTIYSTGKVCNPNQPCILLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLYE	181
Db	121	TMTIYSTGKVCNPNQPCILLLEPGLNEIMANSLDYNERLWAWESRSEVGKQLRPLYE	180
QY	182	EYVLKNEANRANHVEDYGVWRGDIYVNGVDYSGQLIEDVEHTFEIPLFHEHLH	241
Db	181	EYVLKNEANRANHVEDYGVWRGDIYVNGVDYSGQLIEDVEHTFEIPLFHEHLH	240
QY	242	AYVRALKNMAYPSYISPIGCLPAHLGDMWGRFWTNLSYITVPFGQKPNIDVTDAMVQA	301
Db	241	AYVRALKNMAYPSYISPIGCLPAHLGDMWGRFWTNLSYITVPFGQKPNIDVTDAMVQA	300
QY	302	WDQRIKFKAERFFVSGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDVGKDFRLMC	361
Db	301	WDQRIKFKAERFFVSGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDVGKDFRLMC	360
QY	362	TKVTMDDFLTAHHEMGIHQYDMAYAAQPFLLRNGANGEGFEAVGEIMSLSAATPKHLKSI	421
Db	361	TKVTMDDFLTAHHEMGIHQYDMAYAAQPFLLRNGANGEGFEAVGEIMSLSAATPKHLKSI	420
QY	422	GLLSPDFQEDNTEINFLKQALITVGTLPFTYMLKRWNVFKGEIPKQWKKWEMK	481

ALIGNMENTS

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Db 421 GLSPDFQEDNETEINFLKQALTIYGTLPFTYMLEKRWVYKGEIPKQDMKKWEMK 480
Qy 482 REIVGVVPEVPHDETCDPASLFHVSNDYSFIRYTRTYLQFOQALCOAAKHEGPLHK 541
Db 481 REIVGVVPEVPHDETCDPASLFHVSNDYSFIRYTRTYLQFOQALCOAAKHEGPLHK 540
Qy 542 CDISNSTEAGOKLFNMLRGSKSPWTLALENVGAKNNVRPLNLYFPELFTWLKQDNK 601
Db 541 CDISNSTEAGOKLFNMLRGSKSPWTLALENVGAKNNVRPLNLYFPELFTWLKQDNK 600
Qy 602 SFVGSWSDWSPYADOSTIKVIRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVKQ 661
Db 601 SFVGSWSDWSPYADOSTIKVIRISLKSALGDKAYENDNEMYLFRSSVAYAMQYFLKVKQ 660
Qy 662 MILFGEEDVRVANKPRISNFVFTAPRNVSDIIPRTEVEKAIRMSRINDAFRLNDNS 721
Db 661 MILFGEEDVRVANKPRISNFVFTAPRNVSDIIPRTEVEKAIRMSRINDAFRLNDNS 720
Qy 722 LEFLGIOTPLGPPNPPVSIWLVFGVVGVIWVGIVILFTGIRDRKKNKARSGENPY 781
Db 721 LEFLGIOTPLGPPNPPVSIWLVFGVVGVIWVGIVILFTGIRDRKKNKARSGENPY 780
Qy 782 ASIDISKGNPNPGFQNTDDVQTSF 805
Db 781 ASIDISKGNPNPGFQNTDDVQTSF 804

RESULT 2
S05238
peptidyl-di-peptidase A (EC 3.4.15.1) precursor, testicular splice form - human
N:Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptid
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999
C:Accession: S05238; A33979
R:Lattion, A.L.; Soubrier, F.; Allegrini, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas, F.
FEBS Lett. 252, 99-104, 1989
A:Title: The testicular transcript of the angiotensin I-converting enzyme encodes for th
A:Reference number: S05238; MUID:89338720
A:Accession: S05238
A:Molecule type: mRNA
A:Residues: 1-732 <LAT>
A:Cross-references: EMBL:X16295; NID:g28264; PIDN:CAA34362.1; PID:g28265
R:Ehlers, M.R.W.; Fox, E.A.; Stridom, D.J.; Riordan, J.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 7741-7745, 1989
A:Title: Molecular cloning of human testicular angiotensin-converting enzyme: the testis
A:Reference number: A33979; MUID:90046871
A:Accession: A33979
A:Molecule type: mRNA
A:Residues: 1-732 <BRL>
A:Cross-references: GB:M26657; NID:g338666; PIDN:AAA60611.1; PID:g338667
A:Experimental source: clones R1.2 and T8B
A:Note: neither the complete nucleic acid sequence nor the complete translation are show
C:Comment: For the renal and pulmonary splice form, see PR:A31759.
C:Genetics:
A:Gene: GDB:DCP1; ACE
A:Cross-references: GDB:119840; OMIM:106180
A:Map position: 17q23-17q23
C:Function:
A:Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypepti
C:Superfamily: mammalian peptidyl-di-peptidase A
C:Keywords: alternative splicing; glycoprotein; metalloproteinase; peptidyl dipeptide hyd
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-732/Product: peptidyl dipeptidase I #status predicted <MAT>
F:686-702/Domain: transmembrane #status predicted <TRM>
F:103,121,140,186,368,617,651/Binding site: carbohydrate (Asn) #status predic
F:414,418,434/Binding site: zinc, catalytic (His, His, Glu) #status predicted
F:415/Active site: Glu #status predicted

Query Match 31.3%; Score 1344; DB 1: Length 732;
Best Local Similarity 41.8%; Pred. No. 7.6e-85;
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;
Qy 15 TAAQS-----TIEEQAKTFLDKFNHEADLFYQSSLASWYNTNTITETSKILLQNMQIA 62
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Db 61 TSAQSNLVTDEAASKFVEEDYRTSQVVNVEYAEANNWYNTNTITETSKILLQNMQIA 120
Qy 63 NNAGDKWSAFKQGSTLAQMYPLQEIQLNTVQLQALQOQSSVLSKSKRLTILNT 122
Db 121 NHT-----LKGQARFQVQNTTIKRIKKVQDLERAAALPAQELKEEYNKILLD 172
Qy 123 MSTITGKVCNPDNPOQCLLLEPLNEIMANSLDYNERLAWESWRSEVQKQLRPIYEE 182
Db 173 METTYSVATVCHPNG--SCIQLEPDLTNVMTSRKYEDLLAWEGWRDKAGRALIQFYPK 230
Qy 183 YVVLKNEWAPANHYEDYGRGDEYVGVNGDYDSRGOLIEDVEHTFEELKPIYELHA 242
Db 231 YVELNQAARLKVGDAGDSRSNYETPSLE-----QDLERLQELQPLYLNLHA 280
Qy 243 YVRAKLMNAY-PSYISPGCLPAHLGLDMGRFWTNLSYLVFPGQKPNIDVTAMVDQA 301
Db 281 YVRALHRHYGAQHINLEGPIPAHLGLNMAQTWSNIYDLVVVPPSPAPSMDTTEAMLKQ 340
Qy 302 WDAORIEKAEKFEVSVGLPNTQGFWMENSLTDCNVQKAVCHPTAWDLCKG-DFRILM 360
Db 341 WTPRMFEKADDDFTSLGLLPVPEPFNKSMLKPTDGRVNVCHASAWDFYNGKDFRIK 400
Qy 361 CTKYTMDELTAHEMIGHIOYDMAYAAQPFLLRNGANEGHFAVGEIMSLSAATPKHLKS 420
Db 401 CTTVNLEDLVVAHEMIGHIOYFMQYKDLPLVALREGANPGFEHAGIDVLALSVSTPKHLHS 460
Qy 421 IGLSPDFQEDNETEINFLKQALTIYGTLPFTYMLEKRWVYKGEIPKQDMKKWEMK 480
Db 461 LNLSSGGSD-EHDINFLMKMALDKIAPFSYLVQDQWRVFDGSIYKENYQEWWSL 519
Qy 481 KREIVGVVPEVPHDETCDPASLFHVSNDYSFIRYTRTYLQFOQALCOAAKHEGPLH 540
Db 520 RLKYGQLCPVPRTQGFDFGAKFHIPSSVPYIRYFVSFIIQFHEALCOAAGTGPLH 579
Qy 541 KCDISNSTEAGOKLFNMLRGSKSPWTLALENVGAKNNVRPLNLYFPELFTWLKQDNK 600
Db 580 KCDIYQKEAGQRLATANKLGFSPRPPEAMQLITGPNNSASAMLSYFKPLLDMLRTENE 639
Qy 601 --NSFVGW-STDWSPYADQS 617
Db 640 LHGEKLGWPOYNTWTPNSARS 659

RESULT 3
A31759
peptidyl-di-peptidase A (EC 3.4.15.1) precursor, renal and pulmonary splice form - hum
N:Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxype
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999
C:Accession: A31759; PQ0004
R:Soubrier, F.; Alhenc-Gelas, F.; Hubert, C.; Allegrini, J.; John, M.; Tregear, G.; C
Proc. Natl. Acad. Sci. U.S.A. 85, 9386-9390, 1988
A:Title: Two putative active centers in human angiotensin I-converting enzyme reveale
A:Reference number: A31759; MUID:89071703
A:Accession: A31759
A:Molecule type: mRNA
A:Residues: 1-1306 <SOU>
A:Cross-references: GB:J04144; NID:g178285; PIDN:AAA51684.1; PID:g178286
A:Experimental source: kidney
A:Note: parts of this sequence, including the amino end of the mature protein, were d
R:Takeuchi, K.; Shimizu, T.; Onishi, N.; Seyama, Y.; Takaku, F.; Yotsumoto, H.
J. Biochem. 106, 442-445, 1989
A:Title: Purification of human lung angiotensin-converting enzyme by high-performance
A:Reference number: PQ0004; MUID:90110025
A:Accession: PQ0004
A:Molecule type: protein
A:Residues: 'XX', 32-34, 'E', 36-37, 'X', 39-41, 'R', 43-46 <TAK>
A:Experimental source: lung
C:Comment: This splice form is found in many tissues, in particular kidney and lung v
A:Gene: GDB:DCP1; ACE
A:Cross-references: GDB:119840; OMIM:106180
```

A:Map position: 17q23-17q23
 C:Function:
 A:Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptides
 A:Note: Plays a role in the control of blood pressure by catalyzing the conversion of an
 C:Superfamily: mammalian peptidyl-dipeptidase A
 C:Keywords: alternative splicing; blood pressure control; glycoprotein; kidney; lung; me
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-1306/Product: peptidyl dipeptidase I #status predicted <MAM>
 F:1260-1276/Domain: transmembrane #status predicted <TRM>
 F:36,54,74,111,146,160,318,445,509,523,677,695,714,760,942,1191,1225/Binding site: carb
 F:350,394/Binding site: zinc (HIS) #status predicted
 F:988,992,1008/Binding site: zinc, catalytic (HIS, HIS, GLU) #status predicted
 F:989/Active site: Glu #status predicted

Query Match 31.2%; Score 1337; DB 1; Length 1306;
 Best Local Similarity 41.7%; Pred. No. 5.6e-84;
 Matches 255; Conservative 118; Mismatches 204; Indels 34; Gaps 9;

Qy 20 TIEQAKTFLDKFNHEADLFQSSLASWNYNTNITEE-----NVQNNNAGDKWSA 71
 Db 644 TDEAKSKFVEEDRTSQVVMNEYAEANWYNTNITTSKILLQKNQJANHT----- 697

Qy 72 FLKEQSTLAQMYPIQIQLVYKQLQALQOQSSVLSSEKSKRLNTILNTMTSTIYSTGK 131
 Db 698 --LKYGTQARKFQVNLQNTTKRIKKVQDLERAAALPAQELBYNKILLDMETTISVAT 755

Qy 132 VCPNDPQECLELLEGLNEMANSIDYNERLWAMESRSEVGKQLRPLYEYVVLKNEMA 191
 Db 756 VCHPNG--SCLEPDLTNMATSRKYEELWAMESRWDKAGRAILQFYKRYVELINQAA 813

Qy 192 RANHYEDYGDYRGDYEYVVDGYDYSRGQLTIEDVEHTFEIKPLYEHLHAYVRALHMA 251
 Db 814 RLNGYVDAGDSRSMYETPSLE-----QDLERLQELQPLYLNLHAYVRALHHR 863

Qy 252 Y-PSYISPIGCLPAHLGDMGRFTNLSYLVPGQPNIDVDAMVDQAWDAQRIFKE 310
 Db 864 YGAQRINLEGPPIAHLGNMAQTSNIYDLVPPSPASMDTTEAMLKOGWTPRRMFE 923

Qy 311 AEKFFSVGLPNNTOGFENSMILTPGYNOKAVCHPTAWDLGKG--DFRILMCTKVTMDDF 369
 Db 924 ADDFTSLGLLPVPPEFNKSMLEKPTDGRVNVCHASAWDFYNGKDFRIKQTVNLEDL 983

Qy 370 LTAHHEGHIQYDMAYAAQPFLLRNGANEGPHEAVGEMSLSAATPKHLKSIGLLSPDFQ 429
 Db 984 VVAHHEGHIQYPMQTKDLPVALRGANPGFHEATGDYALSVSTPKHLNLSLSEGG 1043

Qy 430 EDNETELNFKLQALITVGLTFFYMLKRWMMVKGEIPKQDMKKWEMKREIVGVVE 489
 Db 1044 SD-EHDINFLMKALDKIAFIPFSYLVQWRNRVDFGSIITKENYQEWWSLRLKYQGLCP 1102

Qy 490 PVPHDETYCDPASLPHVNDYSFIYRTLYQFOFQALCOAAKHGGLHKCDISNSTE 549
 Db 1103 PVPTQGDGDFGAKFHIPSVPIRYFVSFIQFQFHEALCRAAGHTGPLHKCDIYQSKE 1162

Qy 550 AGOKLFNMLRLGKSEPTWLALENVYVAKNMNVRPLNLYFEPLFTWLKQDNK--NSFYGV- 606
 Db 1163 AGQRLATAMKLGFSRPPPEAMQLITQPNMSASAMLSYFKPLDLDWLRTENELHCEKLGWP 1222

Qy 607 STDWSPADQS 617
 Db 1223 QYNWTPNSARS 1233

RESULT 4
 A35655
 peptidyl-dipeptidase A (EC 3.4.15.1), testis - mouse
 A:Alternate names: peptidyl-dipeptidase I, testis
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A35655
 R:Howard, T.E.; Shal, S.Y.; Langford, K.G.; Martin, B.M.; Bernstein, K.E.
 Mol. Cell. Biol. 10, 4294-4302, 1990
 A:Title: Transcription of testicular angiotensin-converting enzyme (ACE) is initiated w

A:Reference number: A35655; MUID:90318396
 A:Accession: A35655
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-732 <HOW>
 A:Cross-references: GB:M5333; NID:g191589; PIDN:AAA37149.1; PID:g191590
 C:Superfamily: mammalian peptidyl-dipeptidase A
 C:Keywords: alternative splicing; peptidyl dipeptide hydrolase; transmembrane protein

Query Match 31.1%; Score 1334; DB 1; Length 732;
 Best Local Similarity 42.6%; Pred. No. 3.7e-84;
 Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

Qy 20 TIEQAKTFLDKFNHEADLFQSSLASWNYNTNITEEYVQNNNAGDKWSAFKKEQSTL 79
 Db 69 TDEAKSKFVEEDRTSQVVMNEYAEANWYNTNITIEGSKILLKSTEVSNHTLKGYTR 128

Qy 80 AOMYPLQEIQLVYKQLQALQOQSSVLSSEKSKRLNTILNTMTSTIYSTCKVCPNPQPQ 139
 Db 129 AKTFDVSFNQSSIKRIKKLQNLDRVLPPELEBYNOILLDMETTSLSNICYTNG-- 186

Qy 140 ECLLEPGLNEMANSIDYNERLWAMESRSEVGKQLRPLYEYVVLKNEMARAHYEDY 199
 Db 187 TCMPLDPLTNMATSRKYEELWAMESRWDKAGRAILPFPFKYVEFSNKLAKLNGYDA 246

Qy 200 GDYWRGDEYVVDGYDYSRGQLTIEDVEHTFEIKPLYEHLHAYVRALHMAVPS-YISP 258
 Db 247 GDSWRSYEDNLE-----QDLKLYQELQPLYLNLHAYVRRSLHRYGSEYINL 296

Qy 259 IGCLPAHLGDMGRFTNLSYLVPGQPNIDVDAMVDQAWDAQRIFKEAKKFFVSV 318
 Db 297 DGPIPAHLGNMAQTSNIYDLVPPSPAPNTDATEAMIKOGWTPRRIFKEADNFTSL 356

Qy 319 GLPNNTOGFENSMILTPGYNOKAVCHPTAWDLGKG--DFRILMCTKVTMDDFLTAHHEMG 377
 Db 357 GLLPVPPEFNKSMLEKPTDGRVNVCHASAWDFYNGKDFRIKQTVNLEDL 416

Qy 378 HIQDMAYAAQPFLLRNGANEGPHEAVGEMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
 Db 417 HIQFMQYKDLPTVFREGANPGFHEATGDYALSVSTPKHLNLSLSTE-GSGYEVDIN 475

Qy 438 FLKQALITVGLTFFYMLKRWMMVKGEIPKQDMKKWEMKREIVGVVEVPVPHDETY 497
 Db 476 FLKMAKLDKTAFTFSLDQWRNRVDFGSIITKENYQEWWSLRLKYQGLCPVPRSGD 535

Qy 498 CDPASLPHVNDYSFIYRTLYQFOFQALCOAAKHGGLHKCDISNSTEAGQKLFNM 557
 Db 536 FDPGSKFHPANVPYRYFVSFIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595

Qy 558 LRLCKSEPTWLALENVYVAKNMNVRPLNLYFEPLFTWLKQDNK--NSFYGV-STDWSP 612
 Db 596 MKLGYSRPPPEAMQLITQPNMSASAMNLYFKPLDLDWLRTENELHCEKLGWP 653

RESULT 5
 A34171
 peptidyl-dipeptidase A (EC 3.4.15.1) precursor - mouse
 A:Alternate names: ACE; angiotensin-converting enzyme; carboxypeptidase; dipeptidyl c
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A34171; A29220; A61477
 R:Bernstein, K.E.; Martin, B.M.; Edwards, A.S.; Bernstein, E.A.
 J. Biol. Chem. 264, 11945-11951, 1989
 A:Title: Mouse angiotensin-converting enzyme is a protein composed of two homologous
 A:Reference number: A34171; MUID:89308599
 A:Accession: A34171
 A:Molecule type: mRNA
 A:Residues: 1-1312 <BER>
 A:Cross-references: GB:J04947
 R:Bernstein, K.E.; Martin, B.M.; Bernstein, E.A.; Linton, J.; Striker, L.; Striker, G
 J. Biol. Chem. 263, 11021-11024, 1988
 A:Title: The isolation of angiotensin-converting enzyme cDNA.
 A:Reference number: A29220; MUID:88298730

A:Accession: A29220
A:Molecule type: mRNA
A:Residues: 1-332 <BE2>
A:Cross-references: GB:J03940; NID:g191583; PIDN:AAA37146.1; PID:g191584
R:Bernstein, K.E.; Martin, B.M.; Striker, L.; Striker, G.
Kidney Int. 33, 652-655, 1988
A:Title: Partial protein sequence of mouse and bovine kidney angiotensin converting enzyme
A:Reference number: A61477; MUID:88215372
A:Accession: A61477
A:Status: preliminary
A:Molecule type: protein
A:Residues: 35-54 <BE3>
A:Experimental source: kidney
A:Superfamily: mammalian peptidyl-dipeptidase A
C:Keywords: alternative splicing; blood pressure control; membrane protein; peptidyl-dipeptidase A
F:1-34/Domain: signal sequence status predicted <SIG>
F:35-132/Product: peptidyl dipeptidase I #status predicted <MAT>

Query Match 31.1%; Score 1334; DB 1; Length 1312;
Best Local Similarity 42.6%; Pred. No. 9,2e-84;
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

Oy 20 TIEQAKTFLDKNHEADLFTQSSLASNNYNTNTEENVONMAGDKWAFKQSTL 79
| | | | | : : : : : | | | | | : : : : : |
Db 649 TDEAKADRFQYEDRTAQLLNEYAEANQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 708
| | | | | : : : : : | | | | | : : : : : |
Oy 80 AOMYPLQEIQLNVLKQLQALQNGSSVLSDSKRLNTILNTMTSTIYSTGKVCNPNPQ 139
| | | | | : : : : : | | | | | : : : : : |
Db 709 AKTFDSNFSQNSIKRIKKLQMLDRAVLPPKELEYNQILLDMETIYSLNICYTNG-- 766
| | | | | : : : : : | | | | | : : : : : |
Oy 140 ECLLLEPGLMEIMANSIDYNERLWMSRSEVKGOLRPLYEYVVLKNEMARANHYEDY 199
| | | | | : : : : : | | | | | : : : : : |
Db 767 TCMLEPLDNLNMTSRKYEEELIWAWSRDKVGRAILPPFPKYVFSNKTAKLNGYTD 826
| | | | | : : : : : | | | | | : : : : : |
Oy 200 GYWRGDEYVNGVDYDSRGOLIEDVHEEIKPLYEHLHAYVRKLMNAPS-VISP 258
| | | | | : : : : : | | | | | : : : : : |
Db 827 GDSRSIYESDNE- - - - - QDEKLYQLQPLYNLHAYVRSLHRYGSEYINL 876
| | | | | : : : : : | | | | | : : : : : |
Oy 259 IGCPLPAHLGLDMMGRFWTNLYSLTVFPGOKPNIDVTDAWVQANDAOIRKEAKKFFVS 318
| | | | | : : : : : | | | | | : : : : : |
Db 877 DGPILPAHLGLNMAQWTSNIDYLVAPFSPAPNIDATAMIKQGWTPRRIEKAEDNFFTS 936
| | | | | : : : : : | | | | | : : : : : |
Oy 319 GLPNTQGFENSMILTPDGNOKAVCHPTAWDLGK-DFRILMCTKVTMDDELTAHEMG 377
| | | | | : : : : : | | | | | : : : : : |
Db 937 GLLPVPEFWNKSMLKEPDTGRVVCVCHPSAWDFYNGKDFRIKQCTSVNEDOLVTAHEMG 996
| | | | | : : : : : | | | | | : : : : : |
Oy 378 HIQYDMAYAAQPELLRNGANEGFHEAVGIMSLSAATPKHLKSTGLSPDQEDNETEIN 437
| | | | | : : : : : | | | | | : : : : : |
Db 997 HIQYFMQYKDLPTVFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 1055
| | | | | : : : : : | | | | | : : : : : |
Oy 438 FLKQALTIIVGTLPFTYMLEKRWVFKGEIPKQDQMKKWMKREIYGVVPEVPHDET 497
| | | | | : : : : : | | | | | : : : : : |
Db 1056 FLAKALDKATFAPFSLDQNRVRFVDSITKENYDMSLRILKYQGLCPPVPRSQGD 1115
| | | | | : : : : : | | | | | : : : : : |
Oy 498 CDPASLFHVSNDYSFIRYTRTYQFQFQALCQAAKHEGPHLKDINSSTEAQOKLFNM 557
| | | | | : : : : : | | | | | : : : : : |
Db 1116 FDPGSKFHPANVPYRYFVSFTIQPFQFALCRAAGTGPLHKCDIYQSKAEGKLADA 1175
| | | | | : : : : : | | | | | : : : : : |
Oy 558 LRLGKSEPTLALENVVGAKNMVRPLNLYREPLFTWLKDNK--NSFVGH-STDWSP 612
| | | | | : : : : : | | | | | : : : : : |
Db 1176 MKLGFSKFWPEAKMLITGQPNMSASAMNYPALPTEWLVNRRRHGETLGMPEYNWAP 1233
| | | | | : : : : : | | | | | : : : : : |

RESULT 6
JC2489
peptidyl-dipeptidase A (EC 3.4.15.1) - chicken
N:Alternate names: angiotensin converting enzyme
C:Species: Gallus gallus (chicken)
C:Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 28-May-1999
A:Accession: JC2489
R:Esther, C.R.; Thomas Jr., K.E.; Bernstein, K.E.
Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994
A:Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme found

A:Reference number: JC2489; MUID:95110342
A:Accession: JC2489
A:Molecule type: mRNA
A:Residues: 1-1193 <EST>
A:Cross-references: GB:I40175; NID:g685168; PIDN:AAA75554.1; PID:g994708
R:Bernstein, K.E.; Martin, B.M.; Striker, L.; Striker, G.
Kidney Int. 33, 652-655, 1988
A:Title: Partial protein sequence of mouse and bovine kidney angiotensin converting enzyme
A:Reference number: A61477; MUID:88215372
A:Accession: A61477
A:Status: preliminary
A:Molecule type: protein
A:Residues: 35-54 <BE3>
A:Experimental source: kidney
A:Superfamily: mammalian peptidyl-dipeptidase A
C:Keywords: alternative splicing; blood pressure control; membrane protein; peptidyl-dipeptidase A
F:1-34/Domain: signal sequence status predicted <SIG>
F:35-132/Product: peptidyl dipeptidase I #status predicted <MAT>

Query Match 30.6%; Score 1312; DB 2; Length 1193;
Best Local Similarity 40.4%; Pred. No. 2.6e-82;
Matches 264; Conservative 110; Mismatches 243; Indels 36; Gaps 10;

Oy 22 BEQAKTFLDKNHEADLFTQSSLASNNYNTNTEENVONMAGDKWAFKQSTLQAQ 81
| | | | | : : : : : | | | | | : : : : : |
Db 544 EAQAKFELSEYNSTAEVYVWNAYTEASWEYNTNITDHKEVLEKMLKAMSKHITIEYGMAR 603
| | | | | : : : : : | | | | | : : : : : |
Oy 82 MYPLQEIQLNVLKQLQALQNGSSVLSDSKRLNTILNTMTSTIYSTGKVCNPN--P 138
| | | | | : : : : : | | | | | : : : : : |
Db 604 QFDSDFQDETIVTRILNKLVSLEAALPEDELKEYNTLLSDMETIYSAKVCRENNTFHP 663
| | | | | : : : : : | | | | | : : : : : |
Oy 139 QECLLLEPGLMEIMANSIDYNERLWMSRSEVKGOLRPLYEYVVLKNEMARANHYED 198
| | | | | : : : : : | | | | | : : : : : |
Db 664 ----LDPDLTILATSRDYNELFAWKGMWASGAKIKDKYRYVELSNKAAVLNGYTD 718
| | | | | : : : : : | | | | | : : : : : |
Oy 199 GYWRGDEYVNGVDYDSRGOLIEDVHEEIKPLYEHLHAYVRKLMNAPS-VSPYIS 257
| | | | | : : : : : | | | | | : : : : : |
Db 719 NGATWSLYETPFE- - - - - EDLERLYQLQPLYNLHAYVRSLHRYGSEYINL 768
| | | | | : : : : : | | | | | : : : : : |
Oy 258 IGCPLPAHLGLDMMGRFWTNLYSLTVFPGOKPNIDVTDAWVQANDAOIRKEAKKFFVS 317
| | | | | : : : : : | | | | | : : : : : |
Db 769 LKGPILPAHLGLNMAQWTSNIDYLVAPFSPAPNIDATAMIKQGWTPRRIEKAEDNFFTS 828
| | | | | : : : : : | | | | | : : : : : |
Oy 318 VGLPNTQGFENSMILTPDGNOKAVCHPTAWDLGK-DGRFRLMCTKVTMDDELTAHEMG 376
| | | | | : : : : : | | | | | : : : : : |
Db 829 LGLPMPQFENSMILTPDGNOKAVCHPTAWDLGK-DGRFRLMCTKVTMDDELTAHEMG 888
| | | | | : : : : : | | | | | : : : : : |
Oy 377 HIQYDMAYAAQPELLRNGANEGFHEAVGIMSLSAATPKHLKSTGLSPDQEDNETEIN 436
| | | | | : : : : : | | | | | : : : : : |
Db 889 GHVQYFLYQMDQPTISFRDGNANPGFHEAIGDIMALSVSTPKHLYSLNLLD-OVTNEESDI 947
| | | | | : : : : : | | | | | : : : : : |
Oy 437 NPLKQALTIIVGTLPFTYMLEKRWVFKGEIPKQDQMKKWMKREIYGVVPEVPHDET 496
| | | | | : : : : : | | | | | : : : : : |
Db 948 NPLKQALTIIVGTLPFTYMLEKRWVFKGEIPKQDQMKKWMKREIYGVVPEVPHDET 1007
| | | | | : : : : : | | | | | : : : : : |
Oy 497 YCDPASLFHVSNDYSFIRYTRTYQFQFQALCQAAKHEGPHLKDINSSTEAQOKLFNM 556
| | | | | : : : : : | | | | | : : : : : |
Db 1008 DFDGAKFHPANVPYRYFVSFTIQPFQFALCRAAGTGPLHKCDIYQSKAEGKLGD 1067
| | | | | : : : : : | | | | | : : : : : |
Oy 557 LRLGKSEPTLALENVVGAKNMVRPLNLYREPLFTWLKDNK--NSFVGH-STDWSP 613
| | | | | : : : : : | | | | | : : : : : |
Db 1068 AMKLGFSKFWPEAKMLITGQPNMSASAMNYPALPTEWLVNRRRHGETLGMPEYSWTYP 1127
| | | | | : : : : : | | | | | : : : : : |
Oy 614 ADQSIKVRISLKSALG-----DKAYEWNDNEMYLFRSSVAYAMQYFLKVK 659
| | | | | : : : : : | | | | | : : : : : |
Db 1128 AVTEFHAATDTADFLGMSVGTQKATAGW-----VLLALALVELITSIFLGVK 1175
| | | | | : : : : : | | | | | : : : : : |

RESULT 7
JC2038
peptidyl-dipeptidase A (EC 3.4.15.1) - rat
N:Alternate names: angiotensin converting enzyme; kininase II
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: JC2038
R:Kolke, G.; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 198, 380-386, 1994
A:Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs
A:Reference number: JC2038; MUID:94121658
A:Accession: JC2038
A:Molecule type: mRNA
A:Residues: 1-1313 <KOI>

A;Cross-references: GB:U03734; NID:6437289; PID:AA62111.1; PID:6437290
A;Note: the authors translated the codon ACG for residue 159 as Tyr
C;Comment: This enzyme is a zinc-containing metalloprotease
C;Comment: This enzyme plays a critical role in blood pressure homeostasis and is the target of angiotensin II
C;Superfamily: mammalian peptidyl-di-peptidase A
C;Keywords: alternative splicing; peptidyl-di-peptidase; transmembrane protein; zinc metalloprotease
F;393-400,990-998/Region: catalytic #status predicted
F;1264-1284/Domain: transmembrane #status predicted <WMS>

Query Match	30.5%	Score 1310;	DB 1;
Best Local Similarity	42.0%	Pred. No. 4.2e-82;	Length 1313;
Matches 251;	Conservative 115;	Mismatches 214;	Indels 18;
			Gaps 7;

```

QY 20 TIEQAKTFLDKFNHBAEDLFYQSSLAGWYNTNITEENVOMNNAAGDKWSAFLKEQSTL 79
db 650 TDAKANRFVEEYDRTAKVFNWXYAEANWHYNTNITEGSKILLQKNKEVSNHHTLKYGWTW 709

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```
QY      80 ACMPPLCEIQNLTVKLOLQALQONGSSVLSDEKSKRLNTILNMTSTIYSTGKVCPNDNPQ 139
       1 :  ||| :: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
DB     710 AKTFDVSFNQTIIKKRIIKVQNVDRVLPPPELEEYNQILLDMETTSYVANVCYTNG-- 767
```

QY	140	EC	LL	PE	PL	GL	NE	IM	AN	SD	NR	LE	WA	WE	SW	RS	EV	GK	QL	RP	LE	YE	YV	VV	LK	NE	MA	RAN	HY	ED	Y	199
db	768	TC	LS	EP	DL	NI	MA	TS	RR	KY	EE	LL	WW	KS	DR	KV	GR	AI	LP	FP	KY	YD	FS	SN	KI	AK	IN	GL	YD	SA	827	

QY	200	GDYWRGDDYEVNGVDYISRGQLIEDVHTFEIKLYLHYHLHAYYRAKLMNAYPS-YTSP	258
Db	828	GDYWRSSYESDDLE-----ODLEKLYQLQPLNLHAYYVRRSLRRHHYGSYEYINL	877

[illegible]

QY 319 GLPNMTQGRWENSMLTDCPNVOKAVCHPTANDLKG - DFRILMCTKVTHDDFLTAAHEMG 377

Db 938 GLLPVPEFWNKSMLEKPTDGRVWCHASANDFYNGKDFRIKQCTSVNNEELVIAHHEMG 997

	QY		HIOYMAYAAQPFLLRNGANEGPHEA	GEIYSLSAATPKHLKSTGLLSPDFQEDNEWIN	437
					:
					:
					:
	Db	998	HIOYFMOYKDLPVTFREGANPGFEHIGDVLALS	VSTPKHLHSNLLSSE-GSGYEHDIN	1056

QY 438 FLLKALITVGTLPFTYLEKNRMWVFKEIPTKDOWMKWKEMREIVGVEVPDHEITY 497
 ||| ||| ||| ||| ||| ||| ||| |||
DB 1057 FLMKMALDKIAFIPFSYLIDQNRWRVFDGSTIKENYNQEWWSLRLKYGLCPVPVRSGGD 1116

00	CDPASLIFHNSDYSFIRYVTRLYQFQFOEALCQAAKHIEGLHKDCINSTEAGOKLFNM	557
498	CDPASLIFHNSDYSFIRYVTRLYQFQFOEALCQAAKHIEGLHKDCINSTEAGOKLFNM	557
1117	FDPGSKFHPANVPYIRYFISFIQFQFHEALCRAAGHTGLYKCDIYQSKAACKLLADA	1176

QY
558 LRLGSEPTLALNVVGAKNMVRPLNPEFLTWLKDNK - NSFWGW-STDWSP 612
:: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
dbd 1177 MKLGYSKWPEAMKIITGPNNSASAIMNYFKPLETWLVTENRHGETLGWPBYTWT 1234

RESULT 8
A34402
peptidyl-dipeptidase A (EC 3.4.15.1) precursor, testicular - rabbit

Alternate names: angiotensin I-converting enzyme; dipeptidyl carboxypeptidase I; peptidyl dipeptidase
 Species: oryctolagus cuniculus (domestic rabbit)
 Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C-Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
 C-Accession: A34402; A36232; C18700
 C-Accession: A60724; A36232; C18700

Prakumar, R.S.; Kusari, J.; Roy, S.N.; Soffer, R.L.; Sen, G.C.
J. Biol. Chem. 264, 16754-16758, 1989
A.Tit: Structure of testicular and lens proteinase A
A.Reference number: A34402; MUID:89380303
A.Segmental mosaic isozyme. A segmental mosaic isozyme.

A:Accession: A34402
A:Molecule type: mRNA
A:Residues: 1-737 <KUM>
A:Cross-references: GB:J05041; NID:q164744; PIDN:AAA31153.1; PID:q164745

R. Sen, G.C.: Thekkumkara, T.J.; Kumar, R.S.
J. Cardiovasc. Pharmacol. 16(Suppl.4), S14-S18, 1990
A. Title: Angiotensin-covering enzyme: structural relationship of the testicular and the
A. Reference number: A60724; MUID: 91155372

A:Cross-references: GB:U03734; NID:g437289; PIDN:AAA82111.1; PID:g437290
A>Note: the authors translated the codon ACC for residue 159 as Tyr
C:Comment: This enzyme is a zinc-containing dicarboxy peptidase that cleaves angiotensin I
C:Comment: This enzyme plays a critical role in blood pressure homeostasis and is the ta
C:Superfamily: mammalian peptidyl-di-peptidase A
C:Keywords: alternative splicing; peptidyldipeptide hydrolase; transmembrane protein; z
F:393-400,990-998/Region: catalytic #status predicted
F:1264-1284/Domain: transmembrane #status predicted <TM>

Query Match 30.5%; Score 1310; DB 1; Length 1313;
Best Local Similarity 42.0%; Pred. No. 4.2e-82;
Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;

QY 20 TIEQAKTFLDKKNHRAEDLFYOSSLASWNYNTNITEENVQNMMNAGDKWSAFLEKQSTL 79
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 650 TDEAKANRFVEEYDRTAKVLWNIEYAANWHYNITIEGSKILLQKNKEVSNHTLKVGTV 709

QY 80 AQMPYLQEIQNLTKVLQALQGGSSVLSEDSKSRILNTILNTMTSTIYSTGKKVCNPDPNQ 139
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 710 AKTFDYSNFQNSTIKRIIKVKQNVDRAVLPNPEEYNOQLLDMETTSYVSANYCYTNG-- 767

QY 140 ECLLLPGLNETMANSLDYNERLNWAESRSEVGKQLRLYEYVVLKNEMARANHYEDY 199
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 768 TCLSLSPDLTNIMATSRKKEYELLWWKSWRDKVGRAILPPFPKYVDFSNKIAKLNCYSDA 827

QY 200 GDYWRCGDYEYVGDYISRGQLIEDVEHTFEIKPLHYHLHAYVRAKLMNAYPS-YISP 258
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 828 GDSWRSSYESDDLE-----QDLEKLYQELQPLNLHAYVRRSLHRHRYGSVINL 877

[illegible]

RESULT 9

S35484

peptidyl-dipeptidase A (EC 3.4.15.1) precursor, pulmonary splice form - rabbit

N:Alternate names: angiotensin-converting enzyme; dipeptidyl carboxypeptidase I; kininase

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text.change 10-Sep-1999

C:Accession: S35484; A23455; A18700; A38655; A49726; S17509

R:Thekkumkara T.J.; Livingston III, W.; Kumar, R.S.; Sen, G.C.

Nucleic Acids Res. 20, 683-687, 1992

A:Title: Use of alternative polyadenylation sites for tissue-specific transcription of the

A:Reference number: S35484; MUID:92178960

A:Accession: S35484

A:Molecule type: mRNA

A:Residues: 1-1309 <THE>

A:Cross-references: EMBL:X62551

R:Iwata, K.; Blacher, R.; Soffer, R.L.; Lai, C.Y.

Arch. Biochem. Biophys. 227, 188-201, 1983

A:Reference number: A23455; MUID:84031289

A:Accession: A23455

A:Molecule type: protein

A:Residues: 34-47, 'N', 49-55 <IWA>

A:Experimental source: lung

R:Iwata, K.; Lai, C.Y.; El-Dorri, H.A.; Soffer, R.L.

Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982

A:Title: The NH2- and COOH-terminal sequences of the angiotensin-converting enzyme isozym

A:Reference number: A90107; MUID:83048249

A:Accession: A18700

A:Molecule type: protein

A:Residues: 34-44; 754-755, 'L', 757 <IW2>

R:Kumar, R.S.; Thekkumkara T.J.; Sen, G.C.

J. Biol. Chem. 256, 3854-3862, 1991

A:Title: The mRNAs encoding the two angiotensin-converting isozymes are transcribed from

A:Reference number: A38655; MUID:91139683

A:Accession: A38655

A:Molecule type: DNA

A:Residues: 1-88 <KUM>

A:Cross-references: GB:M58579

R:Ramchandran, R.; Sen G.C.; Misono, K.; Sen, I.

J. Biol. Chem. 269, 2125-2130, 1994

A:Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting enzym

A:Reference number: A49726; MUID:94124568

A:Accession: A49726

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1236-1258 <RAM>

A:Experimental source: testis

R:Kirley, T.L.

Biochem. J. 278, 375-380, 1991

A:Title: The Mg(2+)-ATPase of rabbit skeletal-muscle transverse tubule is a highly glyco

A:Reference number: S17509; MUID:91378880

A:Accession: S17509

A>Status: preliminary

A:Molecule type: protein

A:Residues: 34-55 <KIR>

C:Comment: This enzyme converts angiotensin I to angiotensin II in presence of divalent

C:Superfamily: mammalian peptidyl-dipeptidase A

C:Keywords: alternative splicing; blood pressure control; chloride; glycoprotein; intest

F:1-33/Domain: signal sequence #status predicted <SIG>

F:34-1309/Product: peptidyl-dipeptidase A; pulmonary #status experimental <NAT>

F:59,79,130,322,448,512,680,698,717,945,1194/Binding site: carbohydrate (Asn) (covalent)

Query Match 29.9% Score 1283; DB 1; Length 1309;

Best Local Similarity 40.8%; Pred. No. 3.1e-80;

Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;

QY 20 TIEQAKTEFLDKFNHEADLFYQSSLASWNYNTNITEE-----NVQNNN--AGDKW 69

Db 647 TDEASRFVEEDRSQAVNVEAEANWNYNTNITEASKILLQKNQNTANHTLYGNW 706

QY 70 SAFLKEOSTLAQMPYQAEITLVKQLQALQNGSSVLSEDKSKRLNTILNTMSTIYT 129

Db 8 ILAGLAVCHGATKEIVATEYLNQINKELAKHTNVETEVSWAYASNITDENELRNEISA 67
 QY 68 KWSAFLKQSTLAQMYPLQEIQLNLTQKLOALQOQSSVLSSEDKSKRLNTILNTMTSTIY 127
 Db 68 ENAKELKEVAKDIQFNWRTYGSADVRQPKSLKGTGYSALPABDYAELLVLSAMESNF 127
 QY 128 STGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVCKQLRPLYEEYVVL 186
 Db 128 AKVRVCDYKNSAKCDLSLDPEIEIITKSRDPEELKYVWTQYDKAGTPTTSNEFKYVEL 187
 QY 167 KNEMARAHYEDYDYGWGDYEVNGVGYDYSGQLIEDVEHTFEETKPLYEHLHAYVR 245
 Db 168 NTKSAKLNFTDGAEWLDEYE-----DATFEDQLEAIFEDIKPLYDQVHGIVR 236
 QY 246 AKLNAY-PSYISPTIGCLPAHLGDMGRFWNTNLSYLVPEFGQKPNIDVTDAWYDQAWDA 304
 Db 237 YRLNKFYGDVSVKGTPLPMLHLLGNMMAQOQSSADIIVSPPEKPLVDVSDENVAQGYTP 296
 QY 305 QRIKAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTK 363
 Db 297 LKMFQMGDDFFQSMGLKLPQEFWDKSILEKPPDDGRDLVCHASAWDFYLTDDVRIKQCTR 356
 QY 364 VTMDLTAHEMIGHIOYDAAQAPFLLRNGANGEGHEAVGEIMSLSAATPKHLKISGL 423
 Db 357 VTQDFVTHHEMIGHIQFYQHPFVYRTGANGPFGHEAVGDVLSVSTPKHLERVGL 416
 QY 424 LSPQEDNETEINFLKQALTIYGLTFTYMLKRWVFKGPIPKDQNMKWKMKRE 483
 Db 417 LK-NYVSDNEARINQLFTALDKIVLPFAFTMDKYRWALFRGQADSEWNCFAFKLREE 475
 QY 484 IGVVPEVPVPHDETCDPASLPHVSNDSYFIRYTRTYLQFOFQALCOAA-----KHG 537
 Db 476 YSGIEPPVVRTEKDFDAPAKYHVSADVEYLYLVSTFIQFYKSAKITAGEYVVPNTEY 535
 QY 538 PLHKCDISNSTEAGKLFNMLRLKSEPTWTLALENVYGAKNMVRPLNTFEPLFTWLK 596
 Db 536 PLDNCIDYGSARAGAFHNMLSGASKPWPDALEAFNGERTMTGKATAEYFELRVVLE 594
 RESULT 11
 A57533
 peptidyl-dipectidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila melanogaster)
 N:Alternate names: angiotensin-converting enzyme
 C:Species: Drosophila melanogaster
 C>Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 26-Feb-1998
 C:Accession: A57533
 R:Corneil, M.J.; Williams, T.A.; Lamango, N.S.; Coates, D.; Corvol, P.; Soubrier, F.; H
 J. Biol. Chem. 270, 13613-13619, 1995
 A:Title: Cloning and expression of an evolutionary conserved single-domain angiotensin c
 A:Reference number: A57533; MUID:95293950
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-615 <COR>
 A:Cross-references: GB:U25344
 C:Genetics:
 A:Gene: FlyBase:Anc
 A:Cross-references: FlyBase:FBgn0012037
 C:Superfamily: mammalian peptidyl-dipectidase A
 C:Keywords: peptidyl-dipectidase hydrolase
 Query Match 24.2%; Score 1039; DB 2; Length 615;
 Best Local Similarity 35.8%; Pred. No. 7.2e-64;
 Matches 219; Conservative 120; Mismatches 251; Indels 22; Gaps 9;
 QY 8 LLSLVAVTAQSTIEEQAKTFLOKFNHEADLFYQSSLASWNTNTNTEENVOMNAGD 67
 Db 8 LLATLVATQALVBEIQAEILENLAKRNTNTEAAWAYGNSITDENKKNEISA 67
 QY 68 KWSAFLKQSTLAQMYPLQEIQLNLTQKLOALQOQSSVLSSEDKSKRLNTILNTMTSTIY 127
 Db 68 ELAKFKEVASDTKTQWRYSQSEDUKRPKALTGLGIAALPDDYAEILLDTLSAMESNF 127

QY 128 STGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVCKQLRPLYEEYVVL 186
 Db 128 AKVVCYDKOSTCDLADPEIEEIVISKSDHEELAYWREFYDKAGTAVRSOFERYVEL 187
 QY 187 KNEMARAHYEDYDYGWGDYEVNGVGYDYSGQLIEDVEHTFEETKPLYEHLHAYVR 246
 Db 188 NTKAAKLNFTSGAEAWLDEYE-----DDTFEQOLEDI---FADIRPLLPADPWLCAF 237
 QY 247 KLNAY-PSYISPTIGCLPAHLGDMGRFWNTNLSYLVPEFGQKPNIDVTDAWYDQAWDA 305
 Db 238 RLKHHYGDVYVSTGPIPMHLLGNMMAQOQSSADIIVSPPEKPLVDVSAEMEKQAYTPL 297
 QY 306 RIFKAEKFFVSVGLPNMTQGFWNSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTKV 364
 Db 298 KMFQMGDDFFTSNNLTKLPQDFWDKSIETPTDGRDLVCHASAWDFYLTDDVRIKQCTR 357
 QY 365 TMDDLTAHEMIGHIOYDAAQAPFLLRNGANGEGHEAVGEIMSLSAATPKHLKISGL 424
 Db 358 TDQQLFTVHHEMIGHIQFYQHPFVYRTGANGPFGHEAVGDVLSVSTPKHLKISGL 417
 QY 425 SPQEDNETEINFLKQALTIYGLTFTYMLKRWVFKGPIPKDQNMKWKMKREI 484
 Db 418 K-DYVRDDEARINQLFTALDKIVLPFAFTMDKYRWSLFRGEVDKANMNCFAFKLREY 476
 QY 485 VGVVPEVPVPHDETCDPASLPHVSNDSYFIRYTRTYLQFOFQALC-QAAKH-----EGP 538
 Db 477 SGIEPPVVRSEKDFDAPAKYHVSADVEYLYLVSTFIQFYKSAKITAGQYDNDVLEP 536
 QY 539 LHKCDISNSTEAGKLFNMLRLKSEPTWTLALENVYGAKNMVRPLNTFEPLFTWLKQ 598
 Db 537 LDNCIDYGSARAGAFHNMLSGASKPWPDALEAFNGERTMTGKATAEYFELRVVLEAE 596
 QY 599 N--KNSFVGHST 608
 Db 597 NIKNNVHIGWTT 608
 RESULT 12
 JC5374
 angiotensin-converting enzyme-related protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jul-2000
 C:Accession: JC5374
 R:Taylor, C.A.M.; Coates, D.; Shirras, A.D.
 Gene 181, 191-197, 1996
 A:Title: The Acer gene of Drosophila codes for an angiotensin-converting enzyme homol
 A:Reference number: JC5374; MUID:97128790
 A:Accession: JC5374
 A:Molecule type: mRNA
 A:Residues: 1-630 <TAV>
 A:Cross-references: EMBL:X96913; NID:g1405881; PIDN:CAA65632.1; PID:g1405882
 C:Genetics:
 A:Gene: Acer
 C:Superfamily: mammalian peptidyl-dipectidase A
 Query Match 24.0%; Score 1030; DB 2; Length 630;
 Best Local Similarity 35.6%; Pred. No. 3.1e-63;
 Matches 219; Conservative 113; Mismatches 260; Indels 24; Gaps 10;
 QY 6 WLLLSLVAVTAQSTIEEQAKTFLOKFNHEADLFYQSSLASWNTNTNTEENVOMNNA 65
 Db 16 WLPHGLSMGNSCSASVLE-ARRFELEENQLARRRHEEFLSGYNTNTNTEANRAMTEV 74
 QY 66 GOKWSAFLKEQSTLAQMYPLQEIQLNLTQKLOALQOQSSVLSSEDKSKRLNTILNTMTST 125
 Db 75 YARNAEINLRKLAQIKSSDYQVQSEDADIRRAEHLKSLCASALNADDYLAQNAISSMOT 134
 QY 126 IYSTGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVCKQLRPLYEEYV 184
 Db 135 NTAATVCSYTTNRSDCSLTLEPHIQERUSHSDPAELAWYREWHDKSGTPMRQNFAYV 194
 QY 185 VLKNEMARAHYEDYDYGWGDYEVNGVGYDYSGQLIEDVEHTFEETKPLYEHLHAYV 244

Db 195 RLTKRASOLNGHRSYADYVQVFE-----DPDEFER-----QLDATEFKQLLLYRQLHGYV 244
 QY 245 RAKLMNAY-PSYISPIGCLPAHLGLDGMGRFWTNLYSLITVPFGOKPNIDVTDAMVQAWD 303
 Db 245 RPRURQHYPDVPMAEGNIPISLIGNMWGQSWNELLDLFTYPEKPFVDVKAEMKOGYT 304
 QY 304 AQRIFKAERKFFVSVGLPNMTQGFWNSMLTDPGNVQAVCHPTAWDLGR-GDFRILMCT 362
 Db 305 VQKUFELGDQFQSLGMRALPPSPNNLSVLTRPD-QRVVCHASAWDFYQSDSDVRKMC 363
 QY 363 KVTMDLTAHHEHGHQYDMAYAAQAPFLLRNGANEGFHEAVGEMSLSAATPKHLKSIG 422
 Db 364 EVDSHYFVYVHHGLHQIYLYQYQYPAVYRGAENPFGFHEAVGDIYALSNSAKHLKAIG 423
 QY 423 LLSDFQEDNETEINFLKQALTIVGTPFTYMLEKRWMMVFKGEIPKQDQWKKWMMKMR 482
 Db 424 LIE-NGRDEKSRINQLFKQALSKIVLPFGYAVDKRYAYAVRNELDQSWNCQFQWRS 482
 QY 483 EIVGVVEPVPHDETYCDPASLFHVSNDYSFYRYTLYQFQEQEALCOAAKHGEP----- 538
 Db 483 EFGGVPEPVFTEKDFDPPAKYHIDADVEYLRYFAAHIFQFQHKVLCRKAGQYAPNNSR 542
 QY 539 --LHKCDISNSTEAGQKLFNMLRGKSEPTLALENVVGAKNMVRPLINAYFEPLFTWLK 596
 Db 543 LTLNCDIFGSKAAGRSLSQFLSKGNSRHWKREVLEETGTETMDPAALLEYFEPLYQWLK 602
 QY 597 DONKNSFVGWSTWSP 612
 Db 603 QE--NSRLGVPLWGP 616

RESULT 13
 T15792
 hypothetical protein C42D8.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
 C:Accession: T15792
 R:Hallsworth, K.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid C42D8.
 A:Reference number: 218405
 A:Accession: T15792
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-907 <HAL>
 A:Cross-references: EMBL:U56966; NID:g1293844; PID:g1293847; PIDN:AAA98719.1; GSPDB:GNOO
 A:Experimental source: strain Bristol N2; clone C42D8
 C:Genetics:
 A:Gene: CESP:C42D8.5
 A:Map position: X
 A:Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3

Query Match 15.0%; Score 642.5; DB 2; Length 907;
 Best Local Similarity 27.0%; Pred. No. 3.5e-36;
 Matches 172; Conservative 136; Mismatches 289; Indels 41; Gaps 19;
 QY 2 SSSSWLLSLAVTAQAQSTIEBQAKTFDKFNHEAEDLFYQSSLASWNYNTNITEE- 61
 Db 160 SSNYKTDNLQAPGSIKD--EKLRSWLAGYBAEAIKVLREVALSGRYFNDAASPXLK 217
 QY 62 MNNAGKWSAFLEKSTLAQMYPLQEIQLNLTVKLQALQONGSSVSEDKSKRLNTILN 121
 Db 218 LDEAENVLTMFYRSTSMQAKQFDMASVTDEKVMQLQYVSPFGMSALAPSRFADYSQA 277
 QY 122 TWSTYSTGKVCNPNPQBCILLEPLGELNEIMANSIDYNERLWAWESRSEVKGQLRPLYE 181
 Db 278 ALNRKSDSTICDKVPPPCALQKIDMSIFNFKEDASRLQHLVSYVTATAKS-KPSYN 336
 QY 182 EYVWLKNEMARANHEDYGDYWRGDIYVNG-VDGYDYSRGQLIEDVEHTFEIKPLYEHL 240
 Db 337 NIITISNEGAKLNGFANGAMRSPAFDMSKVKHAEF---DLNKQIDKIYSTIQPFYQLL 393
 QY 241 HAYVRAKLNNAY--PSYISPIGCLPAHLGLDGMGRFWTNLYSLITVPFGOKPNIDVTDAMV 298

Db 394 HAYMRQLAGIYSNPVGLSKDGPPIAHLFGSLDGGDWSAHYEQTAKPFEES--ETPEAML 451
 QY 299 D-----QAWDAORIFKAERKFFVSVGLPNMTQGFWNSMLTDPGNVQAVCHPTAWDL-G 352
 Db 452 SAFNTQNYTTKMFVTAIRYFKSAGFPPLPKSYWTSISIFARVWS-KDMICHAPAALDMRA 510
 QY 353 KGDFTIMCTKVTMDLTAHHEHGHQYDMAYAAQAPFLLRNGANEGFHEAVGEMSLSA 412
 Db 511 PNDFRVAKAQLCEPDFEQAHSLLVQTYQYLYKQDSLLFREQASPVITADANAFAPHL 570
 QY 413 ATPKHLKSLGSLSPDQEDNETE-INFLKQALTIVGTPFTYMLEKRWMMVFKGEIPK 471
 Db 571 TNPHYLSQKLPSEHLDIKDSVIINKYKESLESTKLPFTTIAADNWRYELDFGTVPKN 630
 QY 472 QWKKWMEKREIVGVVEPVPHDETYCDPASLFH--VSNDSYFIRYITRTL-----YQFOF 525
 Db 631 KLNDRWELRNKVEGVSPOQYNTSLD--ALHNSVSQVHS---PATRTLISYVLKFOI 685
 QY 526 QEALCQAA---KHEGPLHKCDISNSTEAGQKLFNMLRGKSEPTLALENVVGAKNMVR 582
 Db 686 LKALCQRELFWLSEG-----CILSEDTT--EKLRETKLGSITWLKALEMISGKGLDAO 739
 QY 583 PLLNYPEPLFTWLKQDNK--NSFVGWSTWSPYADQSI 618
 Db 740 PLLLEYEPLINLRNTNEIDQVVVVGWGDGEGTPTVEEI 777

RESULT 14
 C83696
 hypothetical protein BH0371 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: C83696
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: C83696
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-532 <STO>
 A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04090.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH0371

Query Match 3.7%; Score 157; DB 2; Length 532;
 Best Local Similarity 21.1%; Pred. No. 0.0058;
 Matches 118; Conservative 83; Mismatches 213; Indels 144; Gaps 29;
 QY 22 EQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-NVQNMNAGDKWSAFLEKOS--- 77
 Db 3 EODIERFLSEQNKRVEDLYQPVLLNHHMWATVTEGQESDKHEQSLSEYWAHFSDRSEFQK 62
 QY 78 -----TLAQMYPLQEIQLNLTVKLQALQONGSSVSEDKSKRLNTILNTSTIY 127
 Db 63 VTRPRKIDSLPLMQRRLDLDLHDKMTKNQFE--EGTRQQILSLE--KKISHVTTTPOQV 118
 QY 128 STGKVCNPNPQECILLLEPLGELNEIMANSIDYNERLWAWESRSEVKGQLRPLYEYVVK 187
 Db 119 NGSRVSNNE-----LLDLIRYDLDRHERRKQAWFA-SKEVGKRTKDLLQLIRKR 166
 QY 188 NEMARANHEDYGDYWRGDIYVNGVDGYDSRGQLIEDVEHT---FEEIKPLYEHLHAYV 244
 Db 167 NEVANRLGFETF-----YHMSFATQELDLQETTFAMFETIKKSSDQAFRMI 211
 QY 245 -----RAKLNNAYPSYISPIGCLPAHLGLDGMGRFWTNLYSLITVPFGOK-PNIDVTD 296
 Db 212 KDEIDEBRAKVLTKTKDDLRL-----WDYVDFPFOARSIEHVD- 250
 QY 297 MVQDAWDAQRIFKAERKFFVSVGLPNMTQGFWNSMLTDPGNVQK-AVCHPTAWDLGKGD 355

Db 251 -FDSFYKQDQLBQVVSQTFQAMELP--IDDLKRSDLYPRKKNKPPGFC--TDMD-RRGD 304

QY 356 FRILMCTKVTMDDFLTAHHENGH-IQYDMAYAAQPELLRNGANEGFHEAVGEIMLSAAT 414

Db 305 IRVLLNLDQSMVYTWALLHEFGHAYVEKFDLSRLPELLR-----FH-----SHTLTT 351

QY 415 PRHLKSIGLLS--PDFQB-----DNET-----EINFLKQALTVGTLPTFTYMLEKWRW 461

Db 352 EASALFFGRMYKMAEYERFGIDRETCERIGRMKMLQROM-VVST-----RW 400

QY 462 MV-----FKG---EIPKQDMKKWEMKREIVGVVPEVPHDETYCDPASLFHVS-----N 508

Db 401 MLTFSFEKSLVEDPDQDINALWKKLVEIQYMAP--PEDTGSPPMAAKMHFSLAPVYYQ 458

QY 509 DY-----SFIRYTYRT 519

Db 459 DYLLGEMASQLHHYIKT 476

RESULT 15

AF1310

probable thermostable carboxypeptidases homolog lmo1886 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C;Accession: AF1310

R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blocker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; Maok, C.; Schluerter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AF1310

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-502 <GLA>

A;Cross-references: GB:NC_003210; PIDN:CAC99964.1; PID:g16411339; GSPDB:GN00177

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo1886

C;Superfamily: Thermus aquaticus carboxypeptidase Tag

Query Match 3.6%; Score 154; DB 2; Length 502;

Best Local Similarity 20.14; Pred.No.0.0085;

Matches 138; Conservative 101; Mismatches 215; Indels 192; Gaps 35;

QY 20 TIEQARTPLDKFNHEAEDLFVQSLSASWNT-----ALVYDLRTGAPAKMGESDVIGVLSIEFIENMQTS 59

Db 4 TLEETFLYIKKMALEAL-----ALVYDLRTGAPAKMGESDVIGVLSIEFIENMQTS 59

QY 66 GDKWSAFLEQSTLAQMYPLQEIQNTLVKLOLQALQNGSVLSDEKSKRL-----N 117

Db 60 -EEMAFIAGLN-----QKEMLS-EITRKTEE---SQTYDLNKKIRFSKEYAEVT 106

QY 118 TILNTMTSTIYTGKVCNPDNPQECILLLEPLGLNEIMANSLDYNERLMAWESRSEVGKQLR 177

Db 107 KLYAQAEATWTTAREQN-----DFAAFEPFLTKIL----- 136

QY 178 PLYEYVVLKMANRANHVEDYGDYWRGDEVNGVCGY--DYSRGOLIEDVEHTEEIKP 235

Db 137 -----ENKR-----KEVEYW--GYEENKYDILLDOYEPGVTVSVDLSVEKVR- 177

QY 236 LYEHLHAYVRAKLMNAYSISYISPGICLPAHLGDMGMRFTWNLNLSUTVPPGQKNIDVTD 295

Db 178 --DGIMA-TREKTEN----- 200

QY 296 AMVQDAQDAQRIFKAEKFFVSGLPNMTQCFWENSMULTDPGNVQKAVCHPTAWDLGKD 355

Db 201 TKISEA-----KQKESFIRI-LNKMGDF-----EAGRLDEVY-HPFATGLNTGD 243

QY 356 FRILMCTKVTMDDFLTA-----HHENGHIQY-----DMAAYAAQPELLRNGANEGFHEAVG-- 405

